



#4

# SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Tryggvason, Karl  
Kallunki, Pekka  
Pyke, Charles
- (ii) TITLE OF INVENTION: Laminin Chains: Diagnostic Uses
- (iii) NUMBER OF SEQUENCES: 20
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Fay Sharpe Fagan Minnich & McKee
  - (B) STREET: 1100 Superior Ave, Suite 700
  - (C) CITY: Cleveland
  - (D) STATE: Ohio
  - (E) COUNTRY: USA
  - (F) ZIP: 44114
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: Unknown
  - (B) FILING DATE: 08 January 2001
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 09/663,147
  - (B) FILING DATE: 150-September 2000
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Minnich, Richard, J.
  - (B) REGISTRATION NUMBER: 24,175
  - (C) REFERENCE/DOCKET NUMBER: TRV 20014
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 216-861-5582
  - (B) TELEFAX: 216-241-1666

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligomer primers"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATCACTGA GCAGCTGAAC

20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAGTACCAGA ACCGAGTTCG

20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTGGTTACCA GGCTTGAGAG

20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTACTGCGGA ATCTCACAGC

20



(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TACACTGTTC AACCCAGGGT

20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAACAAGCCC TCTCACTGGT

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGGAGACTG TGCTGATAAG

20

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CATACCTCTC TACATGGCAT

20



(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGTCTCGCTG AATCTCTCTT

20

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTACAAC TAG CATGGTGCCC

20

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5200 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: sig\_peptide
  - (B) LOCATION: 118..183

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 118..3699

- (ix) FEATURE:
  - (A) NAME/KEY: polyA\_site
  - (B) LOCATION: 4433

- (ix) FEATURE:
  - (A) NAME/KEY: polyA\_site
  - (B) LOCATION: 5195

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GACCACCTGA TCGAAGGAAA AGGAAGGCAC AGCGGAGCGC AGAGTGAGAA CCACCAACCG	60
AGGCGCCGGG CAGCGACCCC TGCAGCGGAG ACAGAGACTG AGCGGCCCGG CACCGCC	117
ATG CCT GCG CTC TGG CTG GGC TGC TGC CTC TGC TTC TCG CTC CTC CTG Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu 1 5 10 15	165
CCC GCA GCC CGG GCC ACC TCC AGG AGG GAA GTC TGT GAT TGC AAT GGG Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly 20 25 30	213
AAG TCC AGG CAG TGT ATC TTT GAT CGG GAA CTT CAC AGA CAA ACT GGT Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly 35 40 45	261
AAT GGA TTC CGC TGC CTC AAC TGC AAT GAC AAC ACT GAT GGC ATT CAC Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His 50 55 60	309
TGC GAG AAG TGC AAG AAT GGC TTT TAC CGG CAC AGA GAA AGG GAC CGC Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg 65 70 75 80	357
TGT TTG CCC TGC AAT TGT AAC TCC AAA GGT TCT CTT AGT GCT CGA TGT Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys 85 90 95	405
GAC AAC TCT GGA CGG TGC AGC TGT AAA CCA GGT GTG ACA GGA GCC AGA Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg 100 105 110	453
TGC GAC CGA TGT CTG CCA GGC TTC CAC ATG CTC ACG GAT GCG GGG TGC Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys 115 120 125	501
ACC CAA GAC CAG AGA CTG CTA GAC TCC AAG TGT GAC TGT GAC CCA GCT Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala 130 135 140	549
GGC ATC GCA GGG CCC TGT GAC GCG GGC CGC TGT GTC TGC AAG CCA GCT Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala 145 150 155 160	597
GTT ACT GGA GAA CGC TGT GAT AGG TGT CGA TCA GGT TAC TAT AAT CTG Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu 165 170 175	645
GAT GGG GGG AAC CCT GAG GGC TGT ACC CAG TGT TTC TGC TAT GGG CAT Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His 180 185 190	693
TCA GCC AGC TGC CGC AGC TCT GCA GAA TAC AGT GTC CAT AAG ATC ACC Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr 195 200 205	741
TCT ACC TTT CAT CAA GAT GTT GAT GGC TGG AAG GCT GTC CAA CGA AAT Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn	789

210	215	220	
GGG TCT CCT GCA AAG CTC CAA TGG TCA CAG CGC CAT CAA GAT GTG TTT Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe 225 230 235 240	837		
AGC TCA GCC CAA CGA CTA GAT CCT GTC TAT TTT GTG GCT CCT GCC AAA Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys 245 250 255	885		
TTT CTT GGG AAT CAA CAG GTG AGC TAT GGG CAA AGC CTG TCC TTT GAC Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp 260 265 270	933		
TAC CGT GTG GAC AGA GGA GGC AGA CAC CCA TCT GCC CAT GAT GTG ATC Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile 275 280 285	981		
CTG GAA GGT GCT GGT CTA CGG ATC ACA GCT CCC TTG ATG CCA CTT GGC Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly 290 295 300	1029		
AAG ACA CTG CCT TGT GGG CTC ACC AAG ACT TAC ACA TTC AGG TTA AAT Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn 305 310 315 320	1077		
GAG CAT CCA AGC AAT AAT TGG AGC CCC CAG CTG AGT TAC TTT GAG TAT Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr 325 330 335	1125		
CGA AGG TTA CTG CGG AAT CTC ACA GCC CTC CGC ATC CGA GCT ACA TAT Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr 340 345 350	1173		
GGA GAA TAC AGT ACT GGG TAC ATT GAC AAT GTG ACC CTG ATT TCA GCC Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala 355 360 365	1221		
CGC CCT GTC TCT GGA GCC CCA GCA CCC TGG GTT GAA CAG TGT ATA TGT Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys 370 375 380	1269		
CCT GTT GGG TAC AAG GGG CAA TTC TGC CAG GAT TGT GCT TCT GGC TAC Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr 385 390 395 400	1317		
AAG AGA GAT TCA GCG AGA CTG GGG CCT TTT GGC ACC TGT ATT CCT TGT Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys 405 410 415	1365		
AAC TGT CAA GGG GGA GGG GCC TGT GAT CCA GAC ACA GGA GAT TGT TAT Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr 420 425 430	1413		
TCA GGG GAT GAG AAT CCT GAC ATT GAG TGT GCT GAC TGC CCA ATT GGT Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly 435 440 445	1461		
TTC TAC AAC GAT CCG CAC GAC CCC CGC AGC TGC AAG CCA TGT CCC TGT	1509		

Phe	Tyr	Asn	Asp	Pro	His	Asp	Pro	Arg	Ser	Cys	Lys	Pro	Cys	Pro	Cys		
450						455					460						
CAT	AAC	GGG	TTC	AGC	TGC	TCA	GTG	ATT	CCG	GAG	ACG	GAG	GAG	GTG	GTG	1557	
His	Asn	Gly	Phe	Ser	Cys	Ser	Val	Ile	Pro	Glu	Thr	Glu	Glu	Val	Val		
465					470					475					480		
TGC	AAT	AAC	TGC	CCT	CCC	GGG	GTC	ACC	GGT	GCC	CGC	TGT	GAG	CTC	TGT	1605	
Cys	Asn	Asn	Cys	Pro	Pro	Gly	Val	Thr	Gly	Ala	Arg	Cys	Glu	Leu	Cys		
				485					490					495			
GCT	GAT	GGC	TAC	TTT	GGG	GAC	CCC	TTT	GGT	GAA	CAT	GGC	CCA	GTG	AGG	1653	
Ala	Asp	Gly	Tyr	Phe	Gly	Asp	Pro	Phe	Gly	Glu	His	Gly	Pro	Val	Arg		
			500					505					510				
CCT	TGT	CAG	CCC	TGT	CAA	TGC	AAC	AGC	AAT	GTG	GAC	CCC	AGT	GCC	TCT	1701	
Pro	Cys	Gln	Pro	Cys	Gln	Cys	Asn	Ser	Asn	Val	Asp	Pro	Ser	Ala	Ser		
		515					520					525					
GGG	AAT	TGT	GAC	CGG	CTG	ACA	GGC	AGG	TGT	TTG	AAG	TGT	ATC	CAC	AAC	1749	
Gly	Asn	Cys	Asp	Arg	Leu	Thr	Gly	Arg	Cys	Leu	Lys	Cys	Ile	His	Asn		
	530					535					540						
ACA	GCC	GGC	ATC	TAC	TGC	GAC	CAG	TGC	AAA	GCA	GGC	TAC	TTC	GGG	GAC	1797	
Thr	Ala	Gly	Ile	Tyr	Cys	Asp	Gln	Cys	Lys	Ala	Gly	Tyr	Phe	Gly	Asp		
545					550					555					560		
CCA	TTG	GCT	CCC	AAC	CCA	GCA	GAC	AAG	TGT	CGA	GCT	TGC	AAC	TGT	AAC	1845	
Pro	Leu	Ala	Pro	Asn	Pro	Ala	Asp	Lys	Cys	Arg	Ala	Cys	Asn	Cys	Asn		
				565					570					575			
CCC	ATG	GGC	TCA	GAG	CCT	GTA	GGA	TGT	CGA	AGT	GAT	GGC	ACC	TGT	GTT	1893	
Pro	Met	Gly	Ser	Glu	Pro	Val	Gly	Cys	Arg	Ser	Asp	Gly	Thr	Cys	Val		
			580					585					590				
TGC	AAG	CCA	GGA	TTT	GGT	GGC	CCC	AAC	TGT	GAG	CAT	GGA	GCA	TTC	AGC	1941	
Cys	Lys	Pro	Gly	Phe	Gly	Gly	Pro	Asn	Cys	Glu	His	Gly	Ala	Phe	Ser		
		595					600						605				
TGT	CCA	GCT	TGC	TAT	AAT	CAA	GTG	AAG	ATT	CAG	ATG	GAT	CAG	TTT	ATG	1989	
Cys	Pro	Ala	Cys	Tyr	Asn	Gln	Val	Lys	Ile	Gln	Met	Asp	Gln	Phe	Met		
	610					615					620						
CAG	CAG	CTT	CAG	AGA	ATG	GAG	GCC	CTG	ATT	TCA	AAG	GCT	CAG	GGT	GGT	2037	
Gln	Gln	Leu	Gln	Arg	Met	Glu	Ala	Leu	Ile	Ser	Lys	Ala	Gln	Gly	Gly		
625					630					635					640		
GAT	GGA	GTA	GTA	CCT	GAT	ACA	GAG	CTG	GAA	GGC	AGG	ATG	CAG	CAG	GCT	2085	
Asp	Gly	Val	Val	Pro	Asp	Thr	Glu	Leu	Glu	Gly	Arg	Met	Gln	Gln	Ala		
				645					650					655			
GAG	CAG	GCC	CTT	CAG	GAC	ATT	CTG	AGA	GAT	GCC	CAG	ATT	TCA	GAA	GGT	2133	
Glu	Gln	Ala	Leu	Gln	Asp	Ile	Leu	Arg	Asp	Ala	Gln	Ile	Ser	Glu	Gly		
			660					665					670				
GCT	AGC	AGA	TCC	CTT	GGT	CTC	CAG	TTG	GCC	AAG	GTG	AGG	AGC	CAA	GAG	2181	
Ala	Ser	Arg	Ser	Leu	Gly	Leu	Gln	Leu	Ala	Lys	Val	Arg	Ser	Gln	Glu		
		675					680						685				

AAC AGC TAC CAG AGC CGC CTG GAT GAC CTC AAG ATG ACT GTG GAA AGA Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg 690 695 700	2229
GTT CGG GCT CTG GGA AGT CAG TAC CAG AAC CGA GTT CGG GAT ACT CAC Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His 705 710 715 720	2277
AGG CTC ATC ACT CAG ATG CAG CTG AGC CTG GCA GAA AGT GAA GCT TCC Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser 725 730 735	2325
TTG GGA AAC ACT AAC ATT CCT GCC TCA GAC CAC TAC GTG GGG CCA AAT Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn 740 745 750	2373
GGC TTT AAA AGT CTG GCT CAG GAG GCC ACA AGA TTA GCA GAA AGC CAC Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His 755 760 765	2421
GTT GAG TCA GCC AGT AAC ATG GAG CAA CTG ACA AGG GAA ACT GAG GAC Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp 770 775 780	2469
TAT TCC AAA CAA GCC CTC TCA CTG GTG CGC AAG GCC CTG CAT GAA GGA Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly 785 790 795 800	2517
GTC GGA AGC GGA AGC GGT AGC CCG GAC GGT GCT GTG GTG CAA GGG CTT Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu 805 810 815	2565
GTG GAA AAA TTG GAG AAA ACC AAG TCC CTG GCC CAG CAG TTG ACA AGG Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg 820 825 830	2613
GAG GCC ACT CAA GCG GAA ATT GAA GCA GAT AGG TCT TAT CAG CAC AGT Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser 835 840 845	2661
CTC CGC CTC CTG GAT TCA GTG TCT CCG CTT CAG GGA GTC AGT GAT CAG Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln 850 855 860	2709
TCC TTT CAG GTG GAA GAA GCA AAG AGG ATC AAA CAA AAA GCG GAT TCA Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser 865 870 875 880	2757
CTC TCA AGC CTG GTA ACC AGG CAT ATG GAT GAG TTC AAG CGT ACA CAA Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln 885 890 895	2805
AAG AAT CTG GGA AAC TGG AAA GAA GAA GCA CAG CAG CTC TTA CAG AAT Lys Asn Leu Gly Asn Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn 900 905 910	2853
GGA AAA AGT GGG AGA GAG AAA TCA GAT CAG CTG CTT TCC CGT GCC AAT Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn	2901



915	920	925	
CTT GCT AAA AGC AGA GCA CAA GAA GCA CTG AGT ATG GGC AAT GCC ACT Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr 930 935 940			2949
TTT TAT GAA GTT GAG AGC ATC CTT AAA AAC CTC AGA GAG TTT GAC CTG Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu 945 950 955 960			2997
CAG GTG GAC AAC AGA AAA GCA GAA GCT GAA GAA GCC ATG AAG AGA CTC Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu 965 970 975			3045
TCC TAC ATC AGC CAG AAG GTT TCA GAT GCC AGT GAC AAG ACC CAG CAA Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln 980 985 990			3093
GCA GAA AGA GCC CTG GGG AGC GCT GCT GCT GAT GCA CAG AGG GCA AAG Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys 995 1000 1005			3141
AAT GGG GCC GGG GAG GCC CTG GAA ATC TCC AGT GAG ATT GAA CAG GAG Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln Glu 1010 1015 1020			3189
ATT GGG AGT CTG AAC TTG GAA GCC AAT GTG ACA GCA GAT GGA GCC TTG Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly Ala Leu 1025 1030 1035 1040			3237
GCC ATG GAA AAG GGA CTG GCC TCT CTG AAG AGT GAG ATG AGG GAA GTG Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met Arg Glu Val 1045 1050 1055			3285
GAA GGA GAG CTG GAA AGG AAG GAG CTG GAG TTT GAC ACG AAT ATG GAT Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp Thr Asn Met Asp 1060 1065 1070			3333
GCA GTA CAG ATG GTG ATT ACA GAA GCC CAG AAG GTT GAT ACC AGA GCC Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys Val Asp Thr Arg Ala 1075 1080 1085			3381
AAG AAC GCT GGG GTT ACA ATC CAA GAC ACA CTC AAC ACA TTA GAC GGC Lys Asn Ala Gly Val Thr Ile Gln Asp Thr Leu Asn Thr Leu Asp Gly 1090 1095 1100			3429
CTC CTG CAT CTG ATG GAC CAG CCT CTC AGT GTA GAT GAA GAG GGG CTG Leu Leu His Leu Met Asp Gln Pro Leu Ser Val Asp Glu Glu Gly Leu 1105 1110 1115 1120			3477
GTC TTA CTG GAG CAG AAG CTT TCC CGA GCC AAG ACC CAG ATC AAC AGC Val Leu Leu Glu Gln Lys Leu Ser Arg Ala Lys Thr Gln Ile Asn Ser 1125 1130 1135			3525
CAA CTG CGG CCC ATG ATG TCA GAG CTG GAA GAG AGG GCA CGT CAG CAG Gln Leu Arg Pro Met Met Ser Glu Leu Glu Glu Arg Ala Arg Gln Gln 1140 1145 1150			3573

AGG GGC CAC CTC CAT TTG CTG GAG ACA AGC ATA GAT GGG ATT CTG GCT Arg Gly His Leu His Leu Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala 1155 1160 1165	3621
GAT GTG AAG AAC TTG GAG AAC ATT AGG GAC AAC CTG CCC CCA GGC TGC Asp Val Lys Asn Leu Glu Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys 1170 1175 1180	3669
TAC AAT ACC CAG GCT CTT GAG CAA CAG TGA AGCTGCCATA AATATTTCTC Tyr Asn Thr Gln Ala Leu Glu Gln Gln *	3719
1185 1190	
AACTGAGGTT CTTGGGATAC AGATCTCAGG GCTCGGGAGC CATGTCATGT GAGTGGGTGG	3779
GATGGGGACA TTTGAACATG TTTAATGGGT ATGCTCAGGT CAACTGACCT GACCCCATTC	3839
CTGATCCCAT GGCCAGGTGG TTGTCTTATT GCACCATACT CCTTGCTTCC TGATGCTGGG	3899
CATGAGGCAG ATAGGCACTG GTGTGAGAAT GATCAAGGAT CTGGACCCCA AAGATAGACT	3959
GGATGGAAAG ACAAACTGCA CAGGCAGATG TTTGCCTCAT AATAGTCGTA AGTGGAGTCC	4019
TGGAATTTGG ACAAGTGCTG TTGGGATATA GTCAACTTAT TCTTTGAGTA ATGTGACTAA	4079
AGGAAAAAAC TTTGACTTTG CCCAGGCATG AAATTCTTCC TAATGTCAGA ACAGAGTGCA	4139
ACCCAGTCAC ACTGTGGCCA GTAAAATACT ATTGCCTCAT ATTGTCTCTCT GCAAGCTTCT	4199
TGCTGATCAG AGTTCCTCCT ACTTACAACC CAGGGTGTGA ACATGTTCTC CATTTTCAAG	4259
CTGGAAGAAG TGAGCAGTGT TGGAGTGAGG ACCTGTAAGG CAGGCCCATT CAGAGCTATG	4319
GTGCTTGCTG GTGCCTGCCA CCTTCAAGTT CTGGACCTGG GCATGACATC CTTTCTTTTA	4379
ATGATGCCAT GGCAACTTAG AGATTGCATT TTTATTAAAG CATTTCCTAC CAGCAAAGCA	4439
AATGTTGGGA AAGTATTTAC TTTTTCGGTT TCAAAGTGAT AGAAAAGTGT GGCTTGGGCA	4499
TTGAAAGAGG TAAAATTCTC TAGATTTATT AGTCCTAATT CAATCCTACT TTTCGAACAC	4559
CAAAAATGAT GCGCATCAAT GTATTTTATC TTATTTTCTC AATCTCCTCT CTCTTTCCTC	4619
CACCCATAAT AAGAGAATGT TCCTACTCAC ACTTCAGCTG GGTACATCC ATCCCTCCAT	4679
TCATCCTTCC ATCCATCTTT CCATCCATTA CCTCCATCCA TCCTTCCAAC ATATATTTAT	4739
TGAGTACCTA CTGTGTGCCA GGGGCTGGTG GGACAGTGGT GACATAGTCT CTGCCCTCAT	4799
AGAGTTGATT GTCTAGTGAG GAAGACAAGC ATTTTAAAAA AATAAATTTA AACTTACAAA	4859
CTTTGTTTGT CACAAGTGGT GTTTATTGCA ATAACCGCTT GGTTTGCAAC CTCTTTGCTC	4919
AACAGAACAT ATGTTGCAAG ACCCTCCCAT GGGCACTGAG TTTGGCAAGG ATGACAGAGC	4979
TCTGGGTTGT GCACATTTCT TTGCATTCCA GCGTCACTCT GTGCCTTCTA CAACTGATTG	5039
CAACAGACTG TTGAGTTATG ATAACACCAG TGGGAATTGC TGGAGGAACC AGAGGCACTT	5099
CCACCTTGGC TGGGAAGACT ATGGTGCTGC CTTGCTTCTG TATTTCTCTG GATTTTCCTG	5159

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu
 1           5           10           15

Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly
 20           25           30

Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly
 35           40           45

Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His
 50           55           60

Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg
 65           70           75           80

Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys
 85           90           95

Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg
100           105           110

Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys
115           120           125

Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala
130           135           140

Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala
145           150           155           160

Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu
165           170           175

Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His
180           185           190

Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr
195           200           205

Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn
210           215           220

Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe
225           230           235           240

Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys

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245								250				255			
Phe	Leu	Gly	Asn	Gln	Gln	Val	Ser	Tyr	Gly	Gln	Ser	Leu	Ser	Phe	Asp
			260					265					270		
Tyr	Arg	Val	Asp	Arg	Gly	Gly	Arg	His	Pro	Ser	Ala	His	Asp	Val	Ile
			275					280					285		
Leu	Glu	Gly	Ala	Gly	Leu	Arg	Ile	Thr	Ala	Pro	Leu	Met	Pro	Leu	Gly
			290					295					300		
Lys	Thr	Leu	Pro	Cys	Gly	Leu	Thr	Lys	Thr	Tyr	Thr	Phe	Arg	Leu	Asn
			305					310					315		
Glu	His	Pro	Ser	Asn	Asn	Trp	Ser	Pro	Gln	Leu	Ser	Tyr	Phe	Glu	Tyr
			325					330					335		
Arg	Arg	Leu	Leu	Arg	Asn	Leu	Thr	Ala	Leu	Arg	Ile	Arg	Ala	Thr	Tyr
			340					345					350		
Gly	Glu	Tyr	Ser	Thr	Gly	Tyr	Ile	Asp	Asn	Val	Thr	Leu	Ile	Ser	Ala
			355					360					365		
Arg	Pro	Val	Ser	Gly	Ala	Pro	Ala	Pro	Trp	Val	Glu	Gln	Cys	Ile	Cys
			370					375					380		
Pro	Val	Gly	Tyr	Lys	Gly	Gln	Phe	Cys	Gln	Asp	Cys	Ala	Ser	Gly	Tyr
			385					390					395		
Lys	Arg	Asp	Ser	Ala	Arg	Leu	Gly	Pro	Phe	Gly	Thr	Cys	Ile	Pro	Cys
			405					410					415		
Asn	Cys	Gln	Gly	Gly	Gly	Ala	Cys	Asp	Pro	Asp	Thr	Gly	Asp	Cys	Tyr
			420					425					430		
Ser	Gly	Asp	Glu	Asn	Pro	Asp	Ile	Glu	Cys	Ala	Asp	Cys	Pro	Ile	Gly
			435					440					445		
Phe	Tyr	Asn	Asp	Pro	His	Asp	Pro	Arg	Ser	Cys	Lys	Pro	Cys	Pro	Cys
			450					455					460		
His	Asn	Gly	Phe	Ser	Cys	Ser	Val	Ile	Pro	Glu	Thr	Glu	Glu	Val	Val
			465					470					475		
Cys	Asn	Asn	Cys	Pro	Pro	Gly	Val	Thr	Gly	Ala	Arg	Cys	Glu	Leu	Cys
			485					490					495		
Ala	Asp	Gly	Tyr	Phe	Gly	Asp	Pro	Phe	Gly	Glu	His	Gly	Pro	Val	Arg
			500					505					510		
Pro	Cys	Gln	Pro	Cys	Gln	Cys	Asn	Ser	Asn	Val	Asp	Pro	Ser	Ala	Ser
			515					520					525		
Gly	Asn	Cys	Asp	Arg	Leu	Thr	Gly	Arg	Cys	Leu	Lys	Cys	Ile	His	Asn
			530					535					540		
Thr	Ala	Gly	Ile	Tyr	Cys	Asp	Gln	Cys	Lys	Ala	Gly	Tyr	Phe	Gly	Asp
			545					550					555		
Pro	Leu	Ala	Pro	Asn	Pro	Ala	Asp	Lys	Cys	Arg	Ala	Cys	Asn	Cys	Asn

				565				570				575			
Pro	Met	Gly	Ser	Glu	Pro	Val	Gly	Cys	Arg	Ser	Asp	Gly	Thr	Cys	Val
580				585				590							
Cys	Lys	Pro	Gly	Phe	Gly	Gly	Pro	Asn	Cys	Glu	His	Gly	Ala	Phe	Ser
595				600				605							
Cys	Pro	Ala	Cys	Tyr	Asn	Gln	Val	Lys	Ile	Gln	Met	Asp	Gln	Phe	Met
610				615				620							
Gln	Gln	Leu	Gln	Arg	Met	Glu	Ala	Leu	Ile	Ser	Lys	Ala	Gln	Gly	Gly
625				630				635				640			
Asp	Gly	Val	Val	Pro	Asp	Thr	Glu	Leu	Glu	Gly	Arg	Met	Gln	Gln	Ala
645				650				655							
Glu	Gln	Ala	Leu	Gln	Asp	Ile	Leu	Arg	Asp	Ala	Gln	Ile	Ser	Glu	Gly
660				665				670							
Ala	Ser	Arg	Ser	Leu	Gly	Leu	Gln	Leu	Ala	Lys	Val	Arg	Ser	Gln	Glu
675				680				685							
Asn	Ser	Tyr	Gln	Ser	Arg	Leu	Asp	Asp	Leu	Lys	Met	Thr	Val	Glu	Arg
690				695				700							
Val	Arg	Ala	Leu	Gly	Ser	Gln	Tyr	Gln	Asn	Arg	Val	Arg	Asp	Thr	His
705				710				715				720			
Arg	Leu	Ile	Thr	Gln	Met	Gln	Leu	Ser	Leu	Ala	Glu	Ser	Glu	Ala	Ser
725				730				735							
Leu	Gly	Asn	Thr	Asn	Ile	Pro	Ala	Ser	Asp	His	Tyr	Val	Gly	Pro	Asn
740				745				750							
Gly	Phe	Lys	Ser	Leu	Ala	Gln	Glu	Ala	Thr	Arg	Leu	Ala	Glu	Ser	His
755				760				765							
Val	Glu	Ser	Ala	Ser	Asn	Met	Glu	Gln	Leu	Thr	Arg	Glu	Thr	Glu	Asp
770				775				780							
Tyr	Ser	Lys	Gln	Ala	Leu	Ser	Leu	Val	Arg	Lys	Ala	Leu	His	Glu	Gly
785				790				795				800			
Val	Gly	Ser	Gly	Ser	Gly	Ser	Pro	Asp	Gly	Ala	Val	Val	Gln	Gly	Leu
805				810				815							
Val	Glu	Lys	Leu	Glu	Lys	Thr	Lys	Ser	Leu	Ala	Gln	Gln	Leu	Thr	Arg
820				825				830							
Glu	Ala	Thr	Gln	Ala	Glu	Ile	Glu	Ala	Asp	Arg	Ser	Tyr	Gln	His	Ser
835				840				845							
Leu	Arg	Leu	Leu	Asp	Ser	Val	Ser	Pro	Leu	Gln	Gly	Val	Ser	Asp	Gln
850				855				860							
Ser	Phe	Gln	Val	Glu	Glu	Ala	Lys	Arg	Ile	Lys	Gln	Lys	Ala	Asp	Ser
865				870				875				880			
Leu	Ser	Ser	Leu	Val	Thr	Arg	His	Met	Asp	Glu	Phe	Lys	Arg	Thr	Gln

885										890					895				
Lys	Asn	Leu	Gly	Asn	Trp	Lys	Glu	Glu	Ala	Gln	Gln	Leu	Leu	Gln	Asn				
			900						905					910					
Gly	Lys	Ser	Gly	Arg	Glu	Lys	Ser	Asp	Gln	Leu	Leu	Ser	Arg	Ala	Asn				
		915					920					925							
Leu	Ala	Lys	Ser	Arg	Ala	Gln	Glu	Ala	Leu	Ser	Met	Gly	Asn	Ala	Thr				
	930					935					940								
Phe	Tyr	Glu	Val	Glu	Ser	Ile	Leu	Lys	Asn	Leu	Arg	Glu	Phe	Asp	Leu				
945					950				955						960				
Gln	Val	Asp	Asn	Arg	Lys	Ala	Glu	Ala	Glu	Glu	Ala	Met	Lys	Arg	Leu				
				965					970					975					
Ser	Tyr	Ile	Ser	Gln	Lys	Val	Ser	Asp	Ala	Ser	Asp	Lys	Thr	Gln	Gln				
			980					985					990						
Ala	Glu	Arg	Ala	Leu	Gly	Ser	Ala	Ala	Ala	Asp	Ala	Gln	Arg	Ala	Lys				
		995					1000					1005							
Asn	Gly	Ala	Gly	Glu	Ala	Leu	Glu	Ile	Ser	Ser	Glu	Ile	Glu	Gln	Glu				
	1010					1015					1020								
Ile	Gly	Ser	Leu	Asn	Leu	Glu	Ala	Asn	Val	Thr	Ala	Asp	Gly	Ala	Leu				
1025					1030					1035					1040				
Ala	Met	Glu	Lys	Gly	Leu	Ala	Ser	Leu	Lys	Ser	Glu	Met	Arg	Glu	Val				
				1045					1050					1055					
Glu	Gly	Glu	Leu	Glu	Arg	Lys	Glu	Leu	Glu	Phe	Asp	Thr	Asn	Met	Asp				
			1060					1065					1070						
Ala	Val	Gln	Met	Val	Ile	Thr	Glu	Ala	Gln	Lys	Val	Asp	Thr	Arg	Ala				
			1075				1080						1085						
Lys	Asn	Ala	Gly	Val	Thr	Ile	Gln	Asp	Thr	Leu	Asn	Thr	Leu	Asp	Gly				
	1090					1095					1100								
Leu	Leu	His	Leu	Met	Asp	Gln	Pro	Leu	Ser	Val	Asp	Glu	Glu	Gly	Leu				
1105				1110						1115					1120				
Val	Leu	Leu	Glu	Gln	Lys	Leu	Ser	Arg	Ala	Lys	Thr	Gln	Ile	Asn	Ser				
				1125					1130					1135					
Gln	Leu	Arg	Pro	Met	Met	Ser	Glu	Leu	Glu	Glu	Arg	Ala	Arg	Gln	Gln				
			1140					1145					1150						
Arg	Gly	His	Leu	His	Leu	Leu	Glu	Thr	Ser	Ile	Asp	Gly	Ile	Leu	Ala				
		1155					1160					1165							
Asp	Val	Lys	Asn	Leu	Glu	Asn	Ile	Arg	Asp	Asn	Leu	Pro	Pro	Gly	Cys				
	1170					1175					1180								
Tyr	Asn	Thr	Gln	Ala	Leu	Glu	Gln	Gln											
1185					1190														

(2) INFORMATION FOR SEQ ID NO:14:

(ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 118..3453
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(ix) FEATURE:
      (A) NAME/KEY: polyA_site
      (B) LOCATION: 4296
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GACCACCTGA	TCGAAGGAAA	AGGAAGGCAC	AGCGGAGCGC	AGAGTGAGAA	CCACCAACCG	60
AGGCGCCGGG	CAGCGACCCC	TGCAGCGGAG	ACAGAGACTG	AGCGGCCCGG	CACCGCC	117
ATG CCT GCG CTC TGG CTG GGC TGC TGC CTC TGC TTC TCG CTC CTC CTG	Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu	165				
1195	1200	1205	1210			
CCC GCA GCC CGG GCC ACC TCC AGG AGG GAA GTC TGT GAT TGC AAT GGG	Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly	213				
	1215	1220	1225			
AAG TCC AGG CAG TGT ATC TTT GAT CGG GAA CTT CAC AGA CAA ACT GGT	Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly	261				
	1230	1235	1240			
AAT GGA TTC CGC TGC CTC AAC TGC AAT GAC AAC ACT GAT GGC ATT CAC	Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His	309				
	1245	1250	1255			
TGC GAG AAG TGC AAG AAT GGC TTT TAC CGG CAC AGA GAA AGG GAC CGC	Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg	357				
	1260	1265	1270			
TGT TTG CCC TGC AAT TGT AAC TCC AAA GGT TCT CTT AGT GCT CGA TGT	Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys	405				
1275	1280	1285	1290			
GAC AAC TCT GGA CGG TGC AGC TGT AAA CCA GGT GTG ACA GGA GCC AGA		453				

Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg	
1295 1300 1305	
TGC GAC CGA TGT CTG CCA GGC TTC CAC ATG CTC ACG GAT GCG GGG TGC	501
Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys	
1310 1315 1320	
ACC CAA GAC CAG AGA CTG CTA GAC TCC AAG TGT GAC TGT GAC CCA GCT	549
Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala	
1325 1330 1335	
GGC ATC GCA GGG CCC TGT GAC GCG GGC CGC TGT GTC TGC AAG CCA GCT	597
Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala	
1340 1345 1350	
GTT ACT GGA GAA CGC TGT GAT AGG TGT CGA TCA GGT TAC TAT AAT CTG	645
Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu	
1355 1360 1365 1370	
GAT GGG GGG AAC CCT GAG GGC TGT ACC CAG TGT TTC TGC TAT GGG CAT	693
Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His	
1375 1380 1385	
TCA GCC AGC TGC CGC AGC TCT GCA GAA TAC AGT GTC CAT AAG ATC ACC	741
Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr	
1390 1395 1400	
TCT ACC TTT CAT CAA GAT GTT GAT GGC TGG AAG GCT GTC CAA CGA AAT	789
Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn	
1405 1410 1415	
GGG TCT CCT GCA AAG CTC CAA TGG TCA CAG CGC CAT CAA GAT GTG TTT	837
Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe	
1420 1425 1430	
AGC TCA GCC CAA CGA CTA GAT CCT GTC TAT TTT GTG GCT CCT GCC AAA	885
Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys	
1435 1440 1445 1450	
TTT CTT GGG AAT CAA CAG GTG AGC TAT GGG CAA AGC CTG TCC TTT GAC	933
Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp	
1455 1460 1465	
TAC CGT GTG GAC AGA GGA GGC AGA CAC CCA TCT GCC CAT GAT GTG ATC	981
Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile	
1470 1475 1480	
CTG GAA GGT GCT GGT CTA CGG ATC ACA GCT CCC TTG ATG CCA CTT GGC	1029
Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly	
1485 1490 1495	
AAG ACA CTG CCT TGT GGG CTC ACC AAG ACT TAC ACA TTC AGG TTA AAT	1077
Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn	
1500 1505 1510	
GAG CAT CCA AGC AAT AAT TGG AGC CCC CAG CTG AGT TAC TTT GAG TAT	1125
Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr	
1515 1520 1525 1530	
CGA AGG TTA CTG CGG AAT CTC ACA GCC CTC CGC ATC CGA GCT ACA TAT	1173



Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr	
1535	1540 1545
GGA GAA TAC AGT ACT GGG TAC ATT GAC AAT GTG ACC CTG ATT TCA GCC	1221
Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala	
1550	1555 1560
CGC CCT GTC TCT GGA GCC CCA GCA CCC TGG GTT GAA CAG TGT ATA TGT	1269
Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys	
1565	1570 1575
CCT GTT GGG TAC AAG GGG CAA TTC TGC CAG GAT TGT GCT TCT GGC TAC	1317
Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr	
1580	1585 1590
AAG AGA GAT TCA GCG AGA CTG GGG CCT TTT GGC ACC TGT ATT CCT TGT	1365
Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys	
1595	1600 1605 1610
AAC TGT CAA GGG GGA GGG GCC TGT GAT CCA GAC ACA GGA GAT TGT TAT	1413
Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr	
1615	1620 1625
TCA GGG GAT GAG AAT CCT GAC ATT GAG TGT GCT GAC TGC CCA ATT GGT	1461
Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly	
1630	1635 1640
TTC TAC AAC GAT CCG CAC GAC CCC CGC AGC TGC AAG CCA TGT CCC TGT	1509
Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys	
1645	1650 1655
CAT AAC GGG TTC AGC TGC TCA GTG ATT CCG GAG ACG GAG GAG GTG GTG	1557
His Asn Gly Phe Ser Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val	
1660	1665 1670
TGC AAT AAC TGC CCT CCC GGG GTC ACC GGT GCC CGC TGT GAG CTC TGT	1605
Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys	
1675	1680 1685 1690
GCT GAT GGC TAC TTT GGG GAC CCC TTT GGT GAA CAT GGC CCA GTG AGG	1653
Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg	
1695	1700 1705
CCT TGT CAG CCC TGT CAA TGC AAC AGC AAT GTG GAC CCC AGT GCC TCT	1701
Pro Cys Gln Pro Cys Gln Cys Asn Ser Asn Val Asp Pro Ser Ala Ser	
1710	1715 1720
GGG AAT TGT GAC CGG CTG ACA GGC AGG TGT TTG AAG TGT ATC CAC AAC	1749
Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn	
1725	1730 1735
ACA GCC GGC ATC TAC TGC GAC CAG TGC AAA GCA GGC TAC TTC GGG GAC	1797
Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp	
1740	1745 1750
CCA TTG GCT CCC AAC CCA GCA GAC AAG TGT CGA GCT TGC AAC TGT AAC	1845
Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn	
1755	1760 1765 1770
CCC ATG GGC TCA GAG CCT GTA GGA TGT CGA AGT GAT GGC ACC TGT GTT	1893

Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val	
1775 1780 1785	
TGC AAG CCA GGA TTT GGT GGC CCC AAC TGT GAG CAT GGA GCA TTC AGC	1941
Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly Ala Phe Ser	
1790 1795 1800	
TGT CCA GCT TGC TAT AAT CAA GTG AAG ATT CAG ATG GAT CAG TTT ATG	1989
Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met	
1805 1810 1815	
CAG CAG CTT CAG AGA ATG GAG GCC CTG ATT TCA AAG GCT CAG GGT GGT	2037
Gln Gln Leu Gln Arg Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly	
1820 1825 1830	
GAT GGA GTA GTA CCT GAT ACA GAG CTG GAA GGC AGG ATG CAG CAG GCT	2085
Asp Gly Val Val Pro Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala	
1835 1840 1845 1850	
GAG CAG GCC CTT CAG GAC ATT CTG AGA GAT GCC CAG ATT TCA GAA GGT	2133
Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly	
1855 1860 1865	
GCT AGC AGA TCC CTT GGT CTC CAG TTG GCC AAG GTG AGG AGC CAA GAG	2181
Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu	
1870 1875 1880	
AAC AGC TAC CAG AGC CGC CTG GAT GAC CTC AAG ATG ACT GTG GAA AGA	2229
Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg	
1885 1890 1895	
GTT CGG GCT CTG GGA AGT CAG TAC CAG AAC CGA GTT CGG GAT ACT CAC	2277
Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His	
1900 1905 1910	
AGG CTC ATC ACT CAG ATG CAG CTG AGC CTG GCA GAA AGT GAA GCT TCC	2325
Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser	
1915 1920 1925 1930	
TTG GGA AAC ACT AAC ATT CCT GCC TCA GAC CAC TAC GTG GGG CCA AAT	2373
Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn	
1935 1940 1945	
GGC TTT AAA AGT CTG GCT CAG GAG GCC ACA AGA TTA GCA GAA AGC CAC	2421
Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His	
1950 1955 1960	
GTT GAG TCA GCC AGT AAC ATG GAG CAA CTG ACA AGG GAA ACT GAG GAC	2469
Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp	
1965 1970 1975	
TAT TCC AAA CAA GCC CTC TCA CTG GTG CGC AAG GCC CTG CAT GAA GGA	2517
Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly	
1980 1985 1990	
GTC GGA AGC GGA AGC GGT AGC CCG GAC GGT GCT GTG GTG CAA GGG CTT	2565
Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu	
1995 2000 2005 2010	
GTG GAA AAA TTG GAG AAA ACC AAG TCC CTG GCC CAG CAG TTG ACA AGG	2613

Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg	
2015 2020 2025	
GAG GCC ACT CAA GCG GAA ATT GAA GCA GAT AGG TCT TAT CAG CAC AGT	2661
Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser	
2030 2035 2040	
CTC CGC CTC CTG GAT TCA GTG TCT CCG CTT CAG GGA GTC AGT GAT CAG	2709
Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln	
2045 2050 2055	
TCC TTT CAG GTG GAA GAA GCA AAG AGG ATC AAA CAA AAA GCG GAT TCA	2757
Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser	
2060 2065 2070	
CTC TCA AGC CTG GTA ACC AGG CAT ATG GAT GAG TTC AAG CGT ACA CAA	2805
Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln	
2075 2080 2085 2090	
AAG AAT CTG GGA AAC TGG AAA GAA GAA GCA CAG CAG CTC TTA CAG AAT	2853
Lys Asn Leu Gly Asn Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn	
2095 2100 2105	
GGA AAA AGT GGG AGA GAG AAA TCA GAT CAG CTG CTT TCC CGT GCC AAT	2901
Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn	
2110 2115 2120	
CTT GCT AAA AGC AGA GCA CAA GAA GCA CTG AGT ATG GGC AAT GCC ACT	2949
Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr	
2125 2130 2135	
TTT TAT GAA GTT GAG AGC ATC CTT AAA AAC CTC AGA GAG TTT GAC CTG	2997
Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu	
2140 2145 2150	
CAG GTG GAC AAC AGA AAA GCA GAA GCT GAA GAA GCC ATG AAG AGA CTC	3045
Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu	
2155 2160 2165 2170	
TCC TAC ATC AGC CAG AAG GTT TCA GAT GCC AGT GAC AAG ACC CAG CAA	3093
Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln	
2175 2180 2185	
GCA GAA AGA GCC CTG GGG AGC GCT GCT GCT GAT GCA CAG AGG GCA AAG	3141
Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys	
2190 2195 2200	
AAT GGG GCC GGG GAG GCC CTG GAA ATC TCC AGT GAG ATT GAA CAG GAG	3189
Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln Glu	
2205 2210 2215	
ATT GGG AGT CTG AAC TTG GAA GCC AAT GTG ACA GCA GAT GGA GCC TTG	3237
Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly Ala Leu	
2220 2225 2230	
GCC ATG GAA AAG GGA CTG GCC TCT CTG AAG AGT GAG ATG AGG GAA GTG	3285
Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met Arg Glu Val	
2235 2240 2245 2250	
GAA GGA GAG CTG GAA AGG AAG GAG CTG GAG TTT GAC ACG AAT ATG GAT	3333

Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp Thr Asn Met Asp	
2255	2260 2265
GCA GTA CAG ATG GTG ATT ACA GAA GCC CAG AAG GTT GAT ACC AGA GCC	3381
Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys Val Asp Thr Arg Ala	
2270	2275 2280
AAG AAC GCT GGG GTT ACA ATC CAA GAC ACA CTC AAC ACA TTA GAC GGC	3429
Lys Asn Ala Gly Val Thr Ile Gln Asp Thr Leu Asn Thr Leu Asp Gly	
2285	2290 2295
CTC CTG CAT CTG ATG GGT ATG TGA ACCCACAACC CACAACCTTC CAGCTCCATG	3483
Leu Leu His Leu Met Gly Met *	
2300	2305
CTCCAGGGCT TTGCTCCAGA ACACTCACTA TACCTAGCCC CAGCAAAGGG GAGTCTCAGC	3543
TTTCCTTAAG GATATCAGTA AATGTGCTTT GTTTCAGGC CCAGATAACT TTCGGCAGGT	3603
TCCCTTACAT TTACTGGACC CTGTTTTACC GTTGCTAAGA TGGGTCACCTG AACACCTATT	3663
GCACTTGGGG GTAAAGGTCT GTGGGCCAAA GAACAGGTGT ATATAAGCAA CTTACAGAA	3723
CACGAGACAG CTTGGGAATC CTGCTAAAGA GTCTGGCCTG GACCCTGAGA AGCCAGTGGA	3783
CAGTTTTAAG CAGAGGAATA ACATCACCAC TGTATATTTT AGAAAGATCA CTAGGGCAGC	3843
CGAGTGGAGG AAAGCTTGAA GAGGGGGTTA GAGAGAAGGC AGGTTGAGAC TACTTAAGAT	3903
ATTGTTGAAA TAATTGAAGA GAGAAATGAC AGGAGCCTGC TCTAAGGCAG TAGAATGGTG	3963
GCTGGGAAGA TGTGAAGGAA GATTTTCCCA GTCTGTGAAG TCAAGAATCA CTTGCCGGCC	4023
GGGTGTGGTG GCTCACGCCT GTAATTCTAG CACTTTGGGA GACTGAAGCG GGTGGATCAC	4083
CCGAGGTCAG GAGTTGAAGA CCAGCCTGGC CAACATGGTG AAACCCTGTC TCTACTAAAA	4143
GTACAAAAAT TAGCTGGATG ATGGTGGTGG GCGCCTGTAA TTCCAGCTAC TCAGGAGTCT	4203
GAGGCAGGAG AATCGCTTGA ACCCAGGAGG CGAGGTTACA GTGAGCCAAG ATTGCACCAC	4263
TGCTCTTCCA GCCTGGGAAC AGAGAGACTG CCTAAAAAAA AAAAAAAAAA AAA	4316

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu	
1 5 10 15	
Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly	
20 25 30	

Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly  
 35 45  
 Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His  
 50 55 60  
 Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg  
 65 70 75 80  
 Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys  
 85 90 95  
 Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg  
 100 105 110  
 Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys  
 115 120 125  
 Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala  
 130 135 140  
 Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala  
 145 150 155 160  
 Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu  
 165 170 175  
 Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His  
 180 185 190  
 Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr  
 195 200 205  
 Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn  
 210 215 220  
 Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe  
 225 230 235 240  
 Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys  
 245 250 255  
 Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp  
 260 265 270  
 Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile  
 275 280 285  
 Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly  
 290 295 300  
 Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn  
 305 310 315 320  
 Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr  
 325 330 335  
 Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr  
 340 345 350

Gly	Glu	Tyr	Ser	Thr	Gly	Tyr	Ile	Asp	Asn	Val	Thr	Leu	Ile	Ser	Ala	
		355					360					365				
Arg	Pro	Val	Ser	Gly	Ala	Pro	Ala	Pro	Trp	Val	Glu	Gln	Cys	Ile	Cys	
	370					375					380					
Pro	Val	Gly	Tyr	Lys	Gly	Gln	Phe	Cys	Gln	Asp	Cys	Ala	Ser	Gly	Tyr	
385					390					395					400	
Lys	Arg	Asp	Ser	Ala	Arg	Leu	Gly	Pro	Phe	Gly	Thr	Cys	Ile	Pro	Cys	
			405						410					415		
Asn	Cys	Gln	Gly	Gly	Gly	Ala	Cys	Asp	Pro	Asp	Thr	Gly	Asp	Cys	Tyr	
		420						425					430			
Ser	Gly	Asp	Glu	Asn	Pro	Asp	Ile	Glu	Cys	Ala	Asp	Cys	Pro	Ile	Gly	
	435						440					445				
Phe	Tyr	Asn	Asp	Pro	His	Asp	Pro	Arg	Ser	Cys	Lys	Pro	Cys	Pro	Cys	
450						455					460					
His	Asn	Gly	Phe	Ser	Cys	Ser	Val	Ile	Pro	Glu	Thr	Glu	Glu	Val	Val	
465					470					475					480	
Cys	Asn	Asn	Cys	Pro	Pro	Gly	Val	Thr	Gly	Ala	Arg	Cys	Glu	Leu	Cys	
			485						490					495		
Ala	Asp	Gly	Tyr	Phe	Gly	Asp	Pro	Phe	Gly	Glu	His	Gly	Pro	Val	Arg	
		500						505					510			
Pro	Cys	Gln	Pro	Cys	Gln	Cys	Asn	Ser	Asn	Val	Asp	Pro	Ser	Ala	Ser	
	515						520					525				
Gly	Asn	Cys	Asp	Arg	Leu	Thr	Gly	Arg	Cys	Leu	Lys	Cys	Ile	His	Asn	
530						535					540					
Thr	Ala	Gly	Ile	Tyr	Cys	Asp	Gln	Cys	Lys	Ala	Gly	Tyr	Phe	Gly	Asp	
545					550					555					560	
Pro	Leu	Ala	Pro	Asn	Pro	Ala	Asp	Lys	Cys	Arg	Ala	Cys	Asn	Cys	Asn	
			565					570					575			
Pro	Met	Gly	Ser	Glu	Pro	Val	Gly	Cys	Arg	Ser	Asp	Gly	Thr	Cys	Val	
		580						585					590			
Cys	Lys	Pro	Gly	Phe	Gly	Gly	Pro	Asn	Cys	Glu	His	Gly	Ala	Phe	Ser	
	595						600					605				
Cys	Pro	Ala	Cys	Tyr	Asn	Gln	Val	Lys	Ile	Gln	Met	Asp	Gln	Phe	Met	
610						615					620					
Gln	Gln	Leu	Gln	Arg	Met	Glu	Ala	Leu	Ile	Ser	Lys	Ala	Gln	Gly	Gly	
625					630					635					640	
Asp	Gly	Val	Val	Pro	Asp	Thr	Glu	Leu	Glu	Gly	Arg	Met	Gln	Gln	Ala	
			645						650					655		
Glu	Gln	Ala	Leu	Gln	Asp	Ile	Leu	Arg	Asp	Ala	Gln	Ile	Ser	Glu	Gly	
		660						665					670			

Ala	Ser	Arg	Ser	Leu	Gly	Leu	Gln	Leu	Ala	Lys	Val	Arg	Ser	Gln	Glu	675	680	685
Asn	Ser	Tyr	Gln	Ser	Arg	Leu	Asp	Asp	Leu	Lys	Met	Thr	Val	Glu	Arg	690	695	700
Val	Arg	Ala	Leu	Gly	Ser	Gln	Tyr	Gln	Asn	Arg	Val	Arg	Asp	Thr	His	705	710	715
Arg	Leu	Ile	Thr	Gln	Met	Gln	Leu	Ser	Leu	Ala	Glu	Ser	Glu	Ala	Ser	725	730	735
Leu	Gly	Asn	Thr	Asn	Ile	Pro	Ala	Ser	Asp	His	Tyr	Val	Gly	Pro	Asn	740	745	750
Gly	Phe	Lys	Ser	Leu	Ala	Gln	Glu	Ala	Thr	Arg	Leu	Ala	Glu	Ser	His	755	760	765
Val	Glu	Ser	Ala	Ser	Asn	Met	Glu	Gln	Leu	Thr	Arg	Glu	Thr	Glu	Asp	770	775	780
Tyr	Ser	Lys	Gln	Ala	Leu	Ser	Leu	Val	Arg	Lys	Ala	Leu	His	Glu	Gly	785	790	795
Val	Gly	Ser	Gly	Ser	Gly	Ser	Pro	Asp	Gly	Ala	Val	Val	Gln	Gly	Leu	805	810	815
Val	Glu	Lys	Leu	Glu	Lys	Thr	Lys	Ser	Leu	Ala	Gln	Gln	Leu	Thr	Arg	820	825	830
Glu	Ala	Thr	Gln	Ala	Glu	Ile	Glu	Ala	Asp	Arg	Ser	Tyr	Gln	His	Ser	835	840	845
Leu	Arg	Leu	Leu	Asp	Ser	Val	Ser	Pro	Leu	Gln	Gly	Val	Ser	Asp	Gln	850	855	860
Ser	Phe	Gln	Val	Glu	Glu	Ala	Lys	Arg	Ile	Lys	Gln	Lys	Ala	Asp	Ser	865	870	875
Leu	Ser	Ser	Leu	Val	Thr	Arg	His	Met	Asp	Glu	Phe	Lys	Arg	Thr	Gln	885	890	895
Lys	Asn	Leu	Gly	Asn	Trp	Lys	Glu	Glu	Ala	Gln	Gln	Leu	Leu	Gln	Asn	900	905	910
Gly	Lys	Ser	Gly	Arg	Glu	Lys	Ser	Asp	Gln	Leu	Leu	Ser	Arg	Ala	Asn	915	920	925
Leu	Ala	Lys	Ser	Arg	Ala	Gln	Glu	Ala	Leu	Ser	Met	Gly	Asn	Ala	Thr	930	935	940
Phe	Tyr	Glu	Val	Glu	Ser	Ile	Leu	Lys	Asn	Leu	Arg	Glu	Phe	Asp	Leu	945	950	955
Gln	Val	Asp	Asn	Arg	Lys	Ala	Glu	Ala	Glu	Glu	Ala	Met	Lys	Arg	Leu	965	970	975
Ser	Tyr	Ile	Ser	Gln	Lys	Val	Ser	Asp	Ala	Ser	Asp	Lys	Thr	Gln	Gln	980	985	990

Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys  
995 1000 1005

Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln Glu  
1010 1015 1020

Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly Ala Leu  
1025 1030 1035 1040

Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met Arg Glu Val  
1045 1050 1055

Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp Thr Asn Met Asp  
1060 1065 1070

Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys Val Asp Thr Arg Ala  
1075 1080 1085

Lys Asn Ala Gly Val Thr Ile Gln Asp Thr Leu Asn Thr Leu Asp Gly  
1090 1095 1100

Leu Leu His Leu Met Gly Met  
1105 1110

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligomer primers"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAGCGCAGAG TGAGAACCAC

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligomer primers"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACTGTATTCT GCAGAGCTGC

20



(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligomer primers"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTCCTTTCCCTACCTTG TG

20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TGTGGAAGCCTGGCAGACAT

20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ala	Gly	Thr	Cys	Thr	Thr	Thr	Ala	Thr	Ala	Gly	Gly	Gly	Ala	Gly	Gly	
1			5					10						15		
Thr	Thr	Gly	Gly	Cys	Cys	Ala	Gly	Thr	Cys	Ala	Ala	Thr	Ala	Gly	Gly	
		20						25					30			
Thr	Thr	Ala	Cys	Thr	Thr	Thr	Ala	Thr	Gly	Ala	Gly	Thr	Thr	Gly	Cys	
		35					40					45				
Thr	Ala	Ala	Cys	Cys	Cys	Thr	Gly	Gly	Thr	Gly	Ala	Gly	Cys	Ala	Gly	
	50					55				60						
Gly	Ala	Ala	Gly	Thr	Thr	Ala	Thr	Gly	Thr	Gly	Gly	Ala	Cys	Cys	Ala	
65				70				75						80		
Gly	Gly	Ala	Gly	Ala	Gly	Ala	Ala	Cys	Cys	Cys	Thr	Thr	Gly	Gly		
		85						90					95			

Thr Thr Cys Ala Gly Cys Cys Thr Gly Gly Ala Gly Ala Ala Ala Gly  
 100 105 110  
 Gly Ala Gly Ala Gly Gly Thr Thr Gly Ala Cys Cys Cys Thr Ala Ala  
 115 120 125  
 Ala Cys Thr Gly Gly Ala Gly Gly Gly Thr Gly Gly Ala Gly Ala Gly  
 130 135 140  
 Gly Ala Cys Cys Cys Thr Gly Thr Thr Gly Thr Gly Ala Cys Thr Cys  
 145 150 155 160  
 Thr Cys Cys Gly Ala Cys Thr Gly Ala Cys Thr Thr Gly Thr Cys Thr  
 165 170 175  
 Thr Cys Cys Thr Thr Gly Ala Thr Gly Thr Cys Cys Thr Thr Thr Ala  
 180 185 190  
 Ala Gly Cys Cys Gly Gly Ala Gly Cys Thr Gly Ala Thr Thr Cys Gly  
 195 200 205  
 Gly Gly Cys Thr Gly Cys Thr Gly Cys Cys Thr Thr Ala Thr Thr Thr  
 210 215 220  
 Cys Thr Gly Ala Gly Thr Thr Ala Gly Cys Gly Cys Thr Cys Thr Thr  
 225 230 235 240  
 Ala Ala Gly Ala Thr Thr Gly Gly Gly Cys Cys Thr Cys Cys Cys Ala  
 245 250 255  
 Gly Thr Thr Thr Gly Ala Gly Gly Ala Ala Gly Gly Gly Gly Cys Gly  
 260 265 270  
 Gly Gly Cys Thr Gly Cys Thr Gly Thr Cys Thr Ala Cys Cys Thr Cys  
 275 280 285  
 Thr Gly Thr Gly Ala Ala Thr Cys Thr Gly Cys Cys Cys Thr Gly Gly  
 290 295 300  
 Ala Cys Cys Ala Cys Cys Cys Cys Gly Gly Gly Ala Gly Ala Gly Ala  
 305 310 315 320  
 Ala Gly Gly Ala Gly Gly Gly Cys Thr Cys Cys Gly Gly Gly Gly Ala  
 325 330 335  
 Ala Thr Cys Thr Cys Gly Cys Ala Cys Ala Thr Thr Cys Cys Ala Gly  
 340 345 350  
 Gly Cys Ala Ala Ala Gly Gly Cys Thr Cys Cys Cys Gly Gly Gly Cys  
 355 360 365  
 Cys Gly Cys Ala Gly Cys Cys Thr Cys Thr Gly Thr Gly Cys Cys Ala  
 370 375 380  
 Cys Ala Cys Cys Cys Thr Thr Gly Gly Cys Cys Cys Gly Gly Gly Cys  
 385 390 395 400  
 Cys Ala Gly Gly Thr Gly Thr Gly Cys Gly Cys Cys Cys Thr Cys Cys  
 405 410 415

Thr Cys Gly Cys Thr Gly Cys Gly Ala Gly Gly Gly Gly Gly Ala Gly  
 420 425 430  
 Cys Gly Gly Gly Cys Gly Gly Cys Thr Gly Cys Gly Gly Gly Gly Ala  
 435 440 445  
 Gly Cys Gly Ala Thr Thr Thr Thr Cys Cys Ala Gly Cys Cys Cys Gly  
 450 455 460  
 Gly Thr Thr Thr Gly Thr Gly Cys Thr Cys Thr Gly Thr Gly Thr Gly  
 465 470 475 480  
 Thr Thr Thr Gly Thr Cys Thr Gly Cys Cys Thr Cys Thr Gly Gly Ala  
 485 490 495  
 Gly Gly Gly Cys Thr Gly Gly Gly Thr Cys Cys Thr Cys Cys Thr Thr  
 500 505 510  
 Ala Thr Thr Cys Ala Cys Ala Gly Gly Thr Gly Ala Gly Thr Cys Ala  
 515 520 525  
 Cys Ala Cys Cys Cys Thr Gly Ala Ala Ala Cys Ala Cys Ala Gly Gly  
 530 535 540  
 Cys Thr Cys Thr Cys Thr Thr Cys Cys Thr Gly Thr Cys Ala Gly Gly  
 545 550 555 560  
 Ala Cys Thr Gly Ala Gly Thr Cys Ala Gly Gly Thr Ala Gly Ala Ala  
 565 570 575  
 Gly Ala Gly Thr Cys Gly Ala Thr Ala Ala Ala Ala Cys Cys Ala Cys  
 580 585 590  
 Cys Thr Gly Ala Thr Cys Ala Ala Gly Gly Ala Ala Ala Ala Gly Gly  
 595 600 605  
 Ala Ala Gly Gly Cys Ala Cys Ala Gly Cys Gly Gly Ala Gly Cys Gly  
 610 615 620  
 Cys Ala Gly Ala Gly Thr Gly Ala Gly Ala Ala Cys Cys Ala Cys Cys  
 625 630 635 640  
 Ala Ala Cys Cys Gly Ala Gly Gly Cys Gly Cys Cys Gly Gly Gly Cys  
 645 650 655  
 Ala Gly Cys Gly Ala Cys Cys Cys Cys Thr Gly Cys Ala Gly Cys Gly  
 660 665 670  
 Gly Ala Gly Ala Cys Ala Gly Ala Gly Ala Cys Thr Gly Ala Gly Cys  
 675 680 685  
 Gly Gly Cys Cys Cys Gly Gly Cys Ala Cys Cys Gly Cys Cys Ala Thr  
 690 695 700  
 Gly Cys Cys Thr Gly Cys Gly Cys Thr Cys Thr Gly Gly Cys Thr Gly  
 705 710 715 720